



SEQ ID NO:90  
3684 nucleotides  
DNA  
Arabidopsis thaliana

CDS  
(501)..(557)

(689)..(818)

(1008)..(1114)

(1194)..(1320)

(1469)..(1576)

(1671)..(1786)

(1858)..(1941)

(2040)..(2108)

(2198)..(2269)

(2352)..(2443)

(2545)..(2672)

(2772)..(2873)

(2965)..(3032)

(3122)..(3181)

agcgattcct tagcagaaag gcgtccatt tctctggcgt aaaccaaagg agatccttga 60

actgtttcct gcaccattgc tcttaaaacc cttctccggc acgaattctt ccaaccctgc 120

ttcaccaccg gaacattgag acaaaatctc gacggtgacg ctgaggttga aaaaaccaat 180

cgaaccgcag acgtaccagg aaccgaacca tgtatcaacg ccattgaaga agaagaagaa 240

gaagaagggtg aaaaacgaaa gattgagaat ttgtttgctt tgagcaacca aacctcagga 300

*FIG. 19A*

|   |      |
|---|------|
| aaaaagagtt aaggtgggag tgtctgggtc aaccggttta tatccgggtc aaattaaacc | 360  |
| tcttacagtt aaccgggttt tgtgtttgtg tcgattgttc ataaaagaaa gaagactctt | 420  |
| gtcgtcgatt agtgccaaag ttgaaagttg aaaccttttc tcagaatttt ctgctcagtt | 480  |
| ctgagttttt ttttcccgcc atg gaa atc gac tcc gag aaa att cac gaa agg | 533  |
| Met Glu Ile Asp Ser Glu Lys Ile His Glu Arg                       |      |
| 1 5 10  |      |
| aag caa tcc gat tac aat tcg ctg gtacgaactc tattacttta tcgacttgta  | 587  |
| Lys Gln Ser Asp Tyr Asn Ser Leu                                   |      |
| 15  |      |
| gtgaaagaca aatgtaatca ttcgtggtgg tgactgtttc tacttataag tgtacgggct | 647  |
| agggtttggt atctgattct gagtttttgc aattgaagca g gat gag aga ttc gag | 703  |
| Asp Glu Arg Phe Glu   |      |
| 20  |      |
| ata cag aag gag atg tac aga ggt cag caa tac agt cag att tac ttt   | 751  |
| Ile Gln Lys Glu Met Tyr Arg Gly Gln Gln Tyr Ser Gln Ile Tyr Phe   |      |
| 25 30 35 40   |      |
| gct cgt ctt cat ctc atg aga aca ctt ctc tac tct ctt gct cct act   | 799  |
| Ala Arg Leu His Leu Met Arg Thr Leu Leu Tyr Ser Leu Ala Pro Thr   |      |
| 45 50 55  |      |
| tgg aaa tct cat ttg cct g gtcagtgcct ttgtttctct catatttagc        | 848  |
| Trp Lys Ser His Leu Pro   |      |
| 60  |      |
| acaacaacga agagcagttt ttgagaattt tcttgggtta gatataatta ggtgaaatca | 908  |
| gtgattttta gggatttttg ctatcttatg gattacagtt gagaaagatt gctagtattg | 968  |
| tttaaattat agatctgaat gtgaatttca tttttgcag tg tgt aag gtt ttg     | 1021 |
| Val Cys Lys Val Leu   |      |
| 65  |      |
| gga ctt gaa aaa gga aaa gaa tgc ata att gtg gga acc ttg ttc aaa   | 1069 |
| Gly Leu Glu Lys Gly Lys Glu Cys Ile Ile Val Gly Thr Leu Phe Lys   |      |
| 70 75 80  |      |

FIG. 19B

|   |      |
|---|------|
| cac atg aag ctt aaa cct tgt gtt ctc gat gaa tat tct aaa gag       | 1114 |
| His Met Lys Leu Lys Pro Cys Val Leu Asp Glu Tyr Ser Lys Glu       |      |
| 85 90 95  |      |
| ggtggttttt attaacctct actgtttttt tgagctatgt ctatgctgaa tcaatctgag | 1174 |
| tatatttaac ataatgcag agg tca gtt act ccg ctt gtt aaa cca cat aac  | 1226 |
| Arg Ser Val Thr Pro Leu Val Lys Pro His Asn                       |      |
| 100 105   |      |
| ttt atg cat cct gat gat aat ctg atc ctc gaa gac gag agt ggg aga   | 1274 |
| Phe Met His Pro Asp Asp Asn Leu Ile Leu Glu Asp Glu Ser Gly Arg   |      |
| 110 115 120 125   |      |
| ggt aag ctt gct ggt tcc gca ctt tca cct gcg att tat gtg aca g     | 1320 |
| Val Lys Leu Ala Gly Ser Ala Leu Ser Pro Ala Ile Tyr Val Thr       |      |
| 130 135 140   |      |
| gtattgcaaa tgggttctta ctgtttttac tgtatgattt tttccttctt tacaatgtgg | 1380 |
| caaatcttag agattttgat caagctttcc tctcttaaaa gatgggttct ttaagaaaat | 1440 |
| taacgttgaa gcctcccgtg cattgtag gt gtt gtt gtt gca ctg cat ggg     | 1491 |
| Gly Val Val Val Ala Leu His Gly                                   |      |
| 145   |      |
| aag gaa act aat gct ggt gaa ttc ttt gtt gag gat gta cta gaa gct   | 1539 |
| Lys Glu Thr Asn Ala Gly Glu Phe Phe Val Glu Asp Val Leu Glu Ala   |      |
| 150 155 160   |      |
| ggt tta cca cct cag att gag cgg cct atc gat cta c gtaagtctag      | 1586 |
| Gly Leu Pro Pro Gln Ile Glu Arg Pro Ile Asp Leu                   |      |
| 165 170 175   |      |
| ctatgttctc ttccttttgc taacctcatg gctcaatcat ttctataagc aatctctcat | 1646 |
| gatacatcca tattgcatct gcag ag gaa gat aaa tat gtc gtg tta ttg     | 1696 |
| Gln Glu Asp Lys Tyr Val Val Leu Leu                               |      |
| 180 185   |      |
| tcg ggc ctt tgt att gga agc aaa tcg gct aat ccc ctg cag ttt cag   | 1744 |
| Ser Gly Leu Cys Ile Gly Ser Lys Ser Ala Asn Pro Leu Gln Phe Gln   |      |
| 190 195 200   |      |

*FIG. 19C*

|   |      |
|---|------|
| ctt ctt gtt gac cat ata act ggg cat ctc gga gat gag gag<br>Leu Leu Val Asp His Ile Thr Gly His Leu Gly Asp Glu Glu<br>205 210 215                     | 1786 |
| gttcaaatct cttacttgc aggtgttca acatatttct ttccttaatt tatactttat   | 1846 |
| ggtttgaaca g gaa caa ggc ctt gca gca cag ata gtt cat gta gta att<br>Glu Gln Gly Leu Ala Ala Gln Ile Val His Val Val Ile<br>220 225                    | 1896 |
| gct gga aac tct ttt gaa ttt ccc cgc aaa ctc att aat ggc cag<br>Ala Gly Asn Ser Phe Glu Phe Pro Arg Lys Leu Ile Asn Gly Gln<br>230 235 240             | 1941 |
| gtacttataa cttttgttgc tgatatattc tcagatacag ttccagtaat tatctgcccc   | 2001 |
| agttatgtct tatgatcttt attggttgat cttttag aac ttg gcc tcg aaa gat<br>Asn Leu Ala Ser Lys Asp<br>245  | 2057 |
| caa tcg aca ctg tat gag ccc atc aaa gag ctt gat atc atg tta agc<br>Gln Ser Thr Leu Tyr Glu Pro Ile Lys Glu Leu Asp Ile Met Leu Ser<br>250 255 260 265 | 2105 |
| cag gtcagttaac tggatctacg tgtgtgttat cgatatctat tgagatgaaa<br>Gln   | 2158 |
| gttcaaaactc ctgttttttt tttgttgat tgttttttag ata gct gca gga gtt<br>Ile Ala Ala Gly Val<br>270   | 2212 |
| tca gta gat atc atg cca ggc acg aat gat cca gct aac ttc gca ttg<br>Ser Val Asp Ile Met Pro Gly Thr Asn Asp Pro Ala Asn Phe Ala Leu<br>275 280 285     | 2260 |
| cct cag cag gtctgcaaat acataagaaa cattcaaaat cccgcatttt<br>Pro Gln Gln<br>290   | 2309 |
| gtatcgataa ctctgattca taggcccttc tctttgttc ag cct ctg aat aga<br>Pro Leu Asn Arg  | 2363 |

|   |      |
|---|------|
| tgt ctt ttc cct gga tct tca cct tat aac acc ttc aga tca tgt aca   | 2411 |
| Cys Leu Phe Pro Gly Ser Ser Pro Tyr Asn Thr Phe Arg Ser Cys Thr   |      |
| 295 300 305 310   |      |
| aat cct cac tca ttt gat gtc gat aat atc ag gtagtattat tattaatagt  | 2463 |
| Asn Pro His Ser Phe Asp Val Asp Asn Ile Arg                       |      |
| 315 320   |      |
| tgaatacaat ctctctgatt ttacaacgat aaaattcttg ggtttatctg actgaaaacc | 2523 |
| tcatatgggg gcattttgca g a ttt ctt gga act tct ggt cag aac atc gat | 2575 |
| Phe Leu Gly Thr Ser Gly Gln Asn Ile Asp                           |      |
| 325 330   |      |
| gac ctt ggc aag tac tca gag gct aag agc aag ctt gat ttt gtg gaa   | 2623 |
| Asp Leu Gly Lys Tyr Ser Glu Ala Lys Ser Lys Leu Asp Phe Val Glu   |      |
| 335 340 345   |      |
| aga acg ctg agg tgg aga cat ctt gcc cca act gca cct aat aca ctc g | 2672 |
| Arg Thr Leu Arg Trp Arg His Leu Ala Pro Thr Ala Pro Asn Thr Leu   |      |
| 350 355 360   |      |
| gtaagaattc tccttgccct gcaagattac ttttttgaac taagcccata aaaaaatgat | 2732 |
| cctttgagtt ctatttggtt ttgattcact tgcgtacag gt tgt tat cct ttc     | 2785 |
| Gly Cys Tyr Pro Phe   |      |
| 365   |      |
| acc gat aga gac cct ttc ttg att gaa acc tgc ccg cat gtc tac ttc   | 2833 |
| Thr Asp Arg Asp Pro Phe Leu Ile Glu Thr Cys Pro His Val Tyr Phe   |      |
| 370 375 380   |      |
| gtc ggg aat caa gat aaa tat gac aac cgt ttg ata aag g gtaaaagcac  | 2883 |
| Val Gly Asn Gln Asp Lys Tyr Asp Asn Arg Leu Ile Lys               |      |
| 385 390 395   |      |
| cttacacaga gattagaaat aacattctct tttgtcaaac atcaggcttt aacttttctt | 2943 |
| gggtaaatat gaatgctgca g gg tca gaa ggg cag ctt gtc cgg ttg atc    | 2993 |
| Gly Ser Glu Gly Gln Leu Val Arg Leu Ile                           |      |
| 400 405   |      |

|  |      |
|--|------|
| tgc att cct aag ttc tgt gag acc ggt att gct gtt gcg gtgagtttaa     | 3042 |
| Cys Ile Pro Lys Phe Cys Glu Thr Gly Ile Ala Val Ala                |      |
| 410 415 420  |      |
| aatttgagca gaatttgaga ccatttacc tcatagattg cagattctaa atctcaaaat   | 3102 |
| caccatgtct atttcgcag gtg aac cta aga aat ctg gaa tgt cac act tta   | 3154 |
| Val Asn Leu Arg Asn Leu Glu Cys His Thr Leu                        |      |
| 425 430  |      |
| agc ttt agc act cag ata aac caa tca taacattgag ttgctacttt          | 3201 |
| Ser Phe Ser Thr Gln Ile Asn Gln Ser                                |      |
| 435 440  |      |
| ggtagattat ttctgtctt gaagatgtaa tgttgagctt tttcagtaac acactcctat   | 3261 |
| gttctaacca aatgtttgtt aaaaatcctt tttcttgagt ggaacttcca aatctttgga  | 3321 |
| tatattggta atgctcattg ttttgccta attttctaaa aatctcgaca cgagttctta   | 3381 |
| ggtagtcaca taaaggacaa aaagggccga ccagatagtg tcgtggtcgt tggtcagaag  | 3441 |
| aacgtgaaaa gactgcaaaa ataatcttaa aaaaagcaac aagtgcacag aatctcatgc  | 3501 |
| aatgtctct ctctctcttc tcaacggcta tatccatcca cacttattac attataaaat   | 3561 |
| taattaaatg caataatgta acgcattata ttctccaacg gtccattttc ccgcattttc  | 3621 |
| ctaacccttc ctttataacg caaaacagtt tcattcttcta cacttaacac tttaatcctc | 3681 |
| tct  | 3684 |

SEQ ID NO:92

3684 nucleotides

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(2772)..(2873)

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(3122)..(3181)

agcgattcct tagcagaaag gcgctccatt tctctggcgt aaaccaaagg agatccttga      60

actgtttcct gcaccattgc tcttaaaacc ctctccggc acgaattctt ccaaccctgc      120

ttcaccaccg gaacattgag acaaaatctc gacggtgacg ctgaggttga aaaaaccaat      180

cgaaccgcag acgtaccagg aaccgaacca tgtatcaacg ccattgaaga agaagaagaa      240

gaagaaggta aaaaacgaaa gattgagaat ttgtttgctt tgagcaacca aacctcagga      300

*FIG. 20A*

|   |      |
|---|------|
| aaaaagatt aaggtggag tgtctggtc aaccggtta tatccggtc aaattaaacc      | 360  |
| tcttacagtt aaccgggttt tgtgtttgt tcgattgtc ataaaagaaa gaagactctt   | 420  |
| gtcgtcgatt agtgccaaag ttgaaagttg aaaccttttc tcagaatttt ctgctcagtt | 480  |
| ctgagttttt ttttccgcc atg gaa atc gac tcc gag aaa att cac gaa agg  | 533  |
| Met Glu Ile Asp Ser Glu Lys Ile His Glu Arg                       |      |
| 1 5 10  |      |
| aag caa tcc gat tac aat tcg ctg gtacgaactc tattacttta tcgacttgta  | 587  |
| Lys Gln Ser Asp Tyr Asn Ser Leu                                   |      |
| 15  |      |
| gtgaaagaca aatgtaatca ttcgtggtgg tgactgtttc tacttataag tgtacgggct | 647  |
| agggtttgtt atctgattct gagttttgc aattgaagca g gat gag aga ttc gag  | 703  |
| Asp Glu Arg Phe Glu   |      |
| 20  |      |
| ata cag aag gag atg tac aga ggt cag caa tac agt cag att tac ttt   | 751  |
| Ile Gln Lys Glu Met Tyr Arg Gly Gln Gln Tyr Ser Gln Ile Tyr Phe   |      |
| 25 30 35 40   |      |
| gct cgt ctt cat ctc atg aga aca ctt ctc tac tct ctt gct cct act   | 799  |
| Ala Arg Leu His Leu Met Arg Thr Leu Leu Tyr Ser Leu Ala Pro Thr   |      |
| 45 50 55  |      |
| tgg aaa tct cat ttg cct g gtcagtgtt ttgtttctct catatttagc         | 848  |
| Trp Lys Ser His Leu Pro   |      |
| 60  |      |
| acaacaacga agagcagttt ttgagaattt tcttgggtta gatataatta ggtgaaatca | 908  |
| gtgattttta gggatttttg ctatcttatg gattacagtt gagaaagatt gctagtattg | 968  |
| tttaaattat agatctgaat gtgaatttca tttttgcag tg tgt aag gtt ttg     | 1021 |
| Val Cys Lys Val Leu   |      |
| 65  |      |
| gga ctt gaa aaa gga aaa gaa tgc ata att gtg gga acc ttg ttc aaa   | 1069 |
| Gly Leu Glu Lys Gly Lys Glu Cys Ile Ile Val Gly Thr Leu Phe Lys   |      |
| 70 75 80  |      |

*FIG. 20B*





|   |      |
|---|------|
| ctt ctt gtt gac cat ata act ggg cat ctc gga gat gag gag<br>Leu Leu Val Asp His Ile Thr Gly His Leu Gly Asp Glu Glu<br>205 210 215                     | 1786 |
| gttcaaactc cttaactgc aggtgtgtca acatatttct ttccttaatt tatactttat  | 1846 |
| ggtttgaaca g gaa caa ggc ctt gca gca cag ata gtt cat gta gta att<br>Glu Gln Gly Leu Ala Ala Gln Ile Val His Val Val Ile<br>220 225                    | 1896 |
| gct gga aac tct ttt gaa ttt ccc cgc aaa ctc att aat ggc cag<br>Ala Gly Asn Ser Phe Glu Phe Pro Arg Lys Leu Ile Asn Gly Gln<br>230 235 240             | 1941 |
| gtacttataa cttttgttgc tgatatattc tcagatacag ttccagtaat tatctgcccc   | 2001 |
| agttatgtct tatgatcttt attggttgat ctttgtag aac ttg gcc tcg aaa gat<br>Asn Leu Ala Ser Lys Asp<br>245   | 2057 |
| caa tcg aca ctg tat gag ccc atc aaa gag ctt gat atc atg tta agc<br>Gln Ser Thr Leu Tyr Glu Pro Ile Lys Glu Leu Asp Ile Met Leu Ser<br>250 255 260 265 | 2105 |
| cag gtcagttaac tggatctacg tgtgtgttat cgatatctat tgagatgaaa<br>Gln   | 2158 |
| gttcaaactc ctgttttttt ttttgtggat tgtttttag ata gct gca gga gtt<br>Ile Ala Ala Gly Val<br>270  | 2212 |
| tca gta gat atc atg cca ggc acg aat gat cca gct aac ttc gca ttg<br>Ser Val Asp Ile Met Pro Gly Thr Asn Asp Pro Ala Asn Phe Ala Leu<br>275 280 285     | 2260 |
| cct cag cag gtctgcaaat acataagaaa cattcaaaat cccgcatttt<br>Pro Gln Gln<br>290   | 2309 |
| gtatcgataa ctctgattca taggcccttc tcttttggtc ag cct ctg aat aga<br>Pro Leu Asn Arg   | 2363 |

*FIG. 20D*

|   |      |
|---|------|
| tgt ctt ttc cct gga tct tca cct tat aac acc ttc aga tca tgt aca<br>Cys Leu Phe Pro Gly Ser Ser Pro Tyr Asn Thr Phe Arg Ser Cys Thr<br>295 300 305 310 | 2411 |
| aat cct cac tca ttt gct gtc gat aat atc ag gtatgattat tattaatagt<br>Asn Pro His Ser Phe Ala Val Asp Asn Ile Arg<br>315 320                            | 2463 |
| tgaatacaat ctctctgatt ttacaacgat aaaattcttg ggtttatctg actgaaaacc   | 2523 |
| tcatatgggg gcattttgca g a ttt ctt gga act tct ggt cag aac atc gat<br>Phe Leu Gly Thr Ser Gly Gln Asn Ile Asp<br>325 330                               | 2575 |
| gac ctt ggc aag tac tca gag gct aag agc aag ctt gat ttt gtg gaa<br>Asp Leu Gly Lys Tyr Ser Glu Ala Lys Ser Lys Leu Asp Phe Val Glu<br>335 340 345     | 2623 |
| aga acg ctg agg tgg aga cat ctt gcc cca act gca cct aat aca ctc g<br>Arg Thr Leu Arg Trp Arg His Leu Ala Pro Thr Ala Pro Asn Thr Leu<br>350 355 360   | 2672 |
| gtaagaattc tccttgccct gcaagattac ttttttgaac taagcccata aaaaaatgat   | 2732 |
| cctttgagtt ctatttggtt ttgattcact tgcgtacag gt tgt tat cct ttc<br>Gly Cys Tyr Pro Phe<br>365   | 2785 |
| acc gat aga gac cct ttc ttg att gaa acc tgc ccg cat gtc tac ttc<br>Thr Asp Arg Asp Pro Phe Leu Ile Glu Thr Cys Pro His Val Tyr Phe<br>370 375 380     | 2833 |
| gtc ggg aat caa gat aaa tat gac aac cgt ttg ata aag g gtaaaagcac<br>Val Gly Asn Gln Asp Lys Tyr Asp Asn Arg Leu Ile Lys<br>385 390 395                | 2883 |
| cttacacaga gattagaaat aacattctct ttgtcaaac atcaggcttt aacttttctt  | 2943 |
| gggtaaatat gaatgctgca g gg tca gaa ggg cag ctt gtc cgg ttg atc<br>Gly Ser Glu Gly Gln Leu Val Arg Leu Ile<br>400 405                                  | 2993 |

|   |      |
|---|------|
| tgc att cct aag ttc tgt gag acc ggt att gct gtt gcg gtgagtttaa    | 3042 |
| Cys Ile Pro Lys Phe Cys Glu Thr Gly Ile Ala Val Ala               |      |
| 410 415 420   |      |
| aatttgagca gaatttgaga ccatttaccc tcatagattg cagattctaa atctcaaaat | 3102 |
| caccatgtct atttcgcag gtg aac cta aga aat ctg gaa tgt cac act tta  | 3154 |
| Val Asn Leu Arg Asn Leu Glu Cys His Thr Leu                       |      |
| 425 430   |      |
| agc ttt agc act cag ata aac caa tca taacattgag ttgctacttt         | 3201 |
| Ser Phe Ser Thr Gln Ile Asn Gln Ser                               |      |
| 435 440   |      |
| ggtagattat ttcctgtctt gaagatgtaa tgttgagctt tttcagtaac acactcctat | 3261 |
| gttctaacca aatgtttgtt aaaaatcctt tttcttgagt ggaacttcca aatctttgga | 3321 |
| tatattggta atgctcattg tttgtccta attttctaaa aatctcgaca cgagttctta  | 3381 |
| ggtagtcaca taaaggacaa aaagggccga ccagatagtg tcgtggtcgt tggtcagaag | 3441 |
| aacgtgaaaa gactgcaaaa ataatcttaa aaaaagcaac aagtgcacag aatctcatgc | 3501 |
| aaatgtctct ctctctcttc tcaacggcta tatccatcca cacttattac attataaaat | 3561 |
| taattaaatg caataatgta acgcattata ttctccaacg gtccattttc ccgcatttcc | 3621 |
| ctaacctttc ctttataacg caaaacagtt tcatcttcta cacttaacac tttaatcctc | 3681 |
| tct   | 3684 |